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Conference Abstract

Progress Out of a Pandemic: Global collections, data sharing, and changing standards of practice

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Abstract

The COVID-19 pandemic has disrupted all aspects of our lives, but has also spawned new opportunities. Months of multidisciplinary, global collaboration have explored the connections between natural history collections and COVID-19. Museums have unrivalled (and still largely untapped) potential to contribute data, methods, and expertise to prediction, mitigation, and prevention efforts related to zoonotic disease outbreaks (DiEuliis et al. 2016, Dunnum et al. 2017), and there is a clear need for ongoing collaboration across (at least) microbiology, disease ecology, and natural history collections. In addition, we note that the roadblocks to effective data access and integration related to microbes and their hosts are a microcosm of the larger data landscape; solving these issues in the context of COVID-19—from liberating data from publications to ensuring digital connections between voucher specimens and all derived viral genetic sequences—will improve biodiversity data access and use more broadly.

Efforts since March 2020 have promoted collaboration across disciplines, international boundaries, and continents. At iDigBio, staff updated information about genetic/genomic resources available in US mammal collections; 24 records were added and information enhanced (Cortez and Soltis 2020). The Distributed System of Scientific Collections (DiSSCo) and the Consortium of European Taxonomic Facilities (CETAF) formed a worldwide COVID-19 Task Force (TaF). A US-led group formed the ViralMuse Task Force, working in concert with the TaF.

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Activities of the TaF centered on four areas: building a hub to coalesce knowledge from this group in a central location – including mining mammals-of-the-world literature, improving the metadata shared when publishing sequence data, encouraging virologists to voucher in museum collections, and gathering critical research questions around zoonotic disease from the scientific community. Through an online public event, this TaF shared work to date and critical next steps. Ongoing efforts include further refinement of metadata requirements for deposition of viral genetic data to include host specimen voucher identifiers, development of methods for better integration of bat and pathogen data from the literature and databases, analysis of community surveys, and development of webinars, symposia, and publications to report the work of the TaF.

Members of the ViralMuse group worked to raise awareness of the critical value of and need for museum experts, collections data, and samples in any analyses of zoonotic events. ViralMuse members (Cook et al. 2020) stressed the need for collaborative action to:

- develop guidelines for keeping samples of both pathogens and hosts.
- develop and implement metadata requirements for physical specimens and samples.
- expand investment in infrastructure, both cyber and physical, to support archives of biological materials.
- increase communication and development of new channels of dialogue and collaboration among museum scientists, microbiologists, bioinformaticians, biomedical professionals, and disease ecologists.
- enhance financial support and realize strong leadership from federal agencies, international partners, and private foundations to develop proactive, multi-disciplinary approaches to future pandemics (see also da Silva et al. 2020).

ViralMuse continues to advance these goals. To reach a broader audience, we published an article in *The Conversation (Soltis et al. 2020*). A new project, funded by the US National Science Foundation (NSF), is aimed at enhancing existing published museum specimen data relevant to one potential reservoir of SARS-CoV-2, horseshoe bats (Mast and Paul 2020). NSF has also provided support to foster continued collaboration, infrastructure development, and integration of communities of practice concerning zoonotic diseases (Soltis and Paul 2020).

From a TDWG perspective, issues relating to data access, data standards, and data integration require attention. Methods to liberate data from publications need to be expanded, and proposed metadata requirements for viral genetic sequences need to be implemented by international databases and adopted by the community. A summit on collections management software could help align efforts to both store and share the necessary host-pathogen information in standards-compliant formats that support discovery, access, and citation/attribution. A new and effective communication strategy is

needed to develop an integrated research community (comprising the biodiversity, collections, data science, disease ecology, microbiology, and One Health communities) and to support needed changes in standards of practice (emphasizing vouchering, data standards, and data integration).

Keywords

COVID-19, One Health, museum collections, host-pathogen, integration

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- iDigBio: Integrated Digitized Biocollections Phase 2
- Rapid Creation of a Data Product for the World's Specimens of Horseshoe Bats and Relatives, a Known Reservoir for Coronaviruses
- Infrastructure for Predicting, Understanding, and Mitigating Zoonotic Disease Outbreaks

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